

PF-0599-2 DIV

<110> Yue, Henry
Au-Young, Janice
Patterson, Chandra

<120> CELL JUNCTION PDZ PROTEIN

<130> PF-0599 US

<140> To Be Assigned

<141> Herewith

<160> 3

<170> PERL Program

<210> 1

<211> 233

<212> PRT

<213> Homo sapiens

<220> -

<223> 1974337

<400> 1

Met	Leu	Lys	Pro	Ser	Val	Thr	Ser	Ala	Pro	Thr	Ala	Asp	Met	Ala
1				5					10					15
Thr	Leu	Thr	Val	Val	Gln	Pro	Leu	Thr	Leu	Asp	Arg	Asp	Val	Ala
			20						25					30
Arg	Ala	Ile	Glu	Leu	Leu	Glu	Lys	Leu	Gln	Glu	Ser	Gly	Glu	Val
			35						40					45
Pro	Val	His	Lys	Leu	Gln	Ser	Leu	Lys	Lys	Val	Leu	Gln	Ser	Glu
			50						55					60
Phe	Cys	Thr	Ala	Ile	Arg	Glu	Val	Tyr	Gln	Tyr	Met	His	Glu	Thr
			65						70					75
Ile	Thr	Val	Asn	Gly	Cys	Pro	Glu	Phe	Arg	Ala	Arg	Ala	Thr	Ala
			80						85					90
Lys	Ala	Thr	Val	Ala	Ala	Phe	Ala	Ala	Ser	Glu	Gly	His	Ser	His
			95						100					105
Pro	Arg	Val	Val	Glu	Leu	Pro	Lys	Thr	Asp	Glu	Gly	Leu	Gly	Phe
			110						115					120
Asn	Val	Met	Gly	Gly	Lys	Glu	Gln	Asn	Ser	Pro	Ile	Tyr	Ile	Ser
			125						130					135
Arg	Ile	Ile	Pro	Gly	Gly	Val	Ala	Glu	Arg	His	Gly	Gly	Leu	Lys
			140						145					150
Arg	Gly	Asp	Gln	Leu	Leu	Ser	Val	Asn	Gly	Val	Ser	Val	Glu	Gly
			155						160					165
Glu	His	His	Glu	Lys	Ala	Val	Glu	Leu	Leu	Lys	Ala	Ala	Lys	Asp
			170						175					180
Ser	Val	Lys	Leu	Val	Val	Arg	Tyr	Thr	Pro	Lys	Val	Leu	Glu	Glu
			185						190					195
Met	Glu	Ala	Arg	Phe	Glu	Lys	Leu	Arg	Thr	Ala	Arg	Arg	Arg	Gln
			200						205					210
Gln	Gln	Gln	Leu	Leu	Ile	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln
			215						220					225
Gln	Thr	Gln	Gln	Asn	His	Met	Ser							
			230											

PF-0599-2 DIV

<210> 2
<211> 1396
<212> DNA
<213> Homo sapiens

<220> -
<223> 1974337

<400> 2
cacgcacccg catgcacaca cgtatattct gaccatttta ttagagtgga aagttgaaag 60
gaagcaaccc gccagctaca cccaccacagc gctcctgggg gtggaatagc aaagttctag 120
ggcagagcct tccctcccag agccccggcg tgcagtcgct ctccgatacc tgctcagctc 180
cgcaccgcaa ctgaagatct gccgcgcggg aacagttgcg tctccatctg gctaccaacc 240
cacccaagct ttctttctcca ccaccaccac ctctcttctt tccccctcct cccctcctt 300
tgggtcctcc ctctccaccc ccgcccccaa tctcctcctt tttttctcac tacgagcggt 360
tgctgatgct gaagccgagc gtcacttcgg ctcccacggc agacatggcg acattgacag 420
tgggtccagcc gctcaccctg gacagagatg ttgcaagagc aattgaatta ctggaaaaac 480
tacaggaatc tggagaagta ccagtgcaca agctacaatc cctcaaaaaa gtgcttcaga 540
gtgagttttg tacagctatt cgagagggtg atcaatatat gcatgaaacg ataactgtta 600
atggctgtcc cgaattccgt gcgaggggcaa cagcaaaggc aacagttgca gctttttgcag 660
ctagtgaagg ccactcccac cctcgagtag ttgaactgcc aaagactgat gaaggccttg 720
gttttaaatgt gatgggagga aaggagcaaa attcccccat ttatatctct cgcataattc 780
ctggaggggt ggctgaaaga cccggaggcc tcaaaaagagg agaccagctg ctatcagtga 840
acggagtgag tgtggaagga gaacaccatg agaaagctgt ggaactactc aaggctgcta 900
aagacagcgt caagctgggt gtgcgataca ccccaaaaagt tctggaagaa atggaggctc 960
gctttgaaaa gctacgaaca gccaggcgctc ggcagcagca gcaattgcta attcagcagc 1020
agcaacagca gcagcagcaa caaacacac aaaccacat gtcataggcc cttgagggaa 1080
agctacttga tcaaacatcc gatagtcaca aatttgaaac cgtgcttcag aatcccagca 1140
catagtaaaa gacaacactg ataattatac ctgtcaagaa gctgtgaaca catgggtgat 1200
aaattcttta ccaaggcaac tcaacacctt cttctctctg gcttgaaccg ccatgctca 1260
cgtgggcttt acatacattg accttcatt cactgcagtg ggaattctca gtgtgcagag 1320
ggagaggttt tctagtctgc aaactgaaac agtgtaagaa gaataaagtc tatgactttt 1380
aaataaaaaa aaaaaa 1396

<210> 3
<211> 297
<212> PRT
<213> Caenorhabditis elegans

<220> -
<223> g1685067

<400> 3
Met Gly Leu Lys Gly Phe Thr Gly Ser Phe Gln Gln Ile Arg Gly
1 5 10 15
Leu Leu Arg Pro Pro Lys Asn Leu Pro Phe Arg Gly Ile Phe Arg
20 25 30
Lys Asp Gly Glu Val Val Arg Lys Asp Asp Leu Leu Val Asn Gln
35 40 45
Phe Lys Met Asn Tyr His Pro Gly Leu Asn Val Tyr Tyr Glu Asn
50 55 60
Asp Arg Gly Glu Arg Leu Leu Arg Ala His Cys Asp Gly Ile Val
65 70 75
Arg Ile Ser Gln Glu Lys Cys Asp Pro Asp Tyr Glu Ile Glu Glu
80 85 90
Met Lys Gly Tyr Glu Tyr Arg Lys Asp Val Asp Leu Tyr Lys Met
95 100 105
Thr Phe Asn Met Asp Asn Pro Asp Gly Pro Asn Leu Glu Arg Asp
110 115 120

PF-0599-2 DIV

Val	Gln	Arg	Ile	Leu	Glu	Leu	Met	Glu	His	Val	Gln	Lys	Thr	Gly
				125					130					135
Glu	Val	Asn	Asn	Ala	Lys	Leu	Ala	Ser	Leu	Gln	Gln	Val	Leu	Gln
				140					145					150
Ser	Glu	Phe	Phe	Gly	Ala	Val	Arg	Glu	Val	Tyr	Glu	Thr	Val	Tyr
				155					160					165
Glu	Ser	Ile	Asp	Ala	Asp	Thr	Thr	Pro	Glu	Ile	Lys	Ala	Ala	Ala
				170					175					180
Thr	Ala	Lys	Ala	Thr	Val	Ala	Ala	Phe	Ala	Ala	Ala	Glu	Gly	His
				185					190					195
Ala	His	Pro	Arg	Ile	Val	Glu	Leu	Pro	Lys	Thr	Asp	Gln	Gly	Leu
				200					205					210
Gly	Phe	Asn	Val	Met	Gly	Gly	Lys	Glu	Gln	Asn	Ser	Pro	Ile	Tyr
				215					220					225
Ile	Ser	Arg	Ile	Ile	Pro	Gly	Gly	Val	Ala	Asp	Arg	His	Gly	Gly
				230					235					240
Leu	Lys	Arg	Gly	Asp	Gln	Leu	Ile	Ala	Val	Asn	Gly	Asn	Val	Glu
				245					250					255
Ala	Glu	Cys	His	Glu	Lys	Ala	Val	Asp	Leu	Leu	Lys	Ser	Ala	Val
				260					265					270
Gly	Ser	Val	Lys	Leu	Val	Ile	Arg	Tyr	Met	Pro	Lys	Leu	Leu	Asp
				275					280					285
Glu	Met	Glu	Arg	Arg	Phe	Glu	Arg	Gln	Arg	Ile	Pro			
				290					295					